

**AMENDMENTS TO THE CLAIMS, COMPLETE LISTING OF CLAIMS**  
**IN ASCENDING ORDER WITH STATUS INDICATOR**

Please amend the following claims as indicated.

Claims 1-13 (Canceled).

14. (Canceled).

15. (Canceled).

16. (Currently Amended) A method for determining amino acid sequence of protein or peptide, which comprises

reacting ~~the a metal complex according to claim 17~~ with a protein or peptide (A) of which the amino acid sequence is to be determined, to form a derivative (B) of said metal complex, ~~where the covalent bond of the functional group of the metal complex with the amino group of the N terminal amino acid residue of the protein or peptide (A) or with the carboxyl group of the C terminal amino acid residue of protein or peptide is formed, and~~

analyzing the derivative (B) through mass spectrometry to obtain mass spectrometry data of the derivative (B), and

determining the amino acid sequence of said protein or peptide from the mass spectrometry data,

wherein said metal complex comprises a functional group which has a property of forming a covalent bond with an amino group of an N-terminal amino acid residue of protein or peptide,

wherein the derivative (B) comprises said metal complex covalently bonded via ~~a the~~ functional group on said metal complex to either the amino group of the N-terminal amino acid residue, ~~or the carboxyl group of the C terminal amino acid residue~~ of said protein or peptide (A),

wherein the covalent bond to be formed between the amino group of the N-terminal amino acid residue of protein or peptide and the functional group is not cleaved in a stage of ionization in mass spectrometry, and

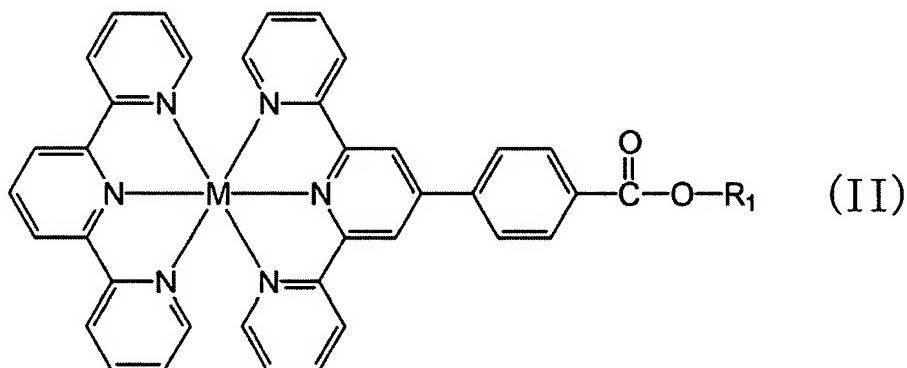
wherein the metal complex is represented by the following formula (I):



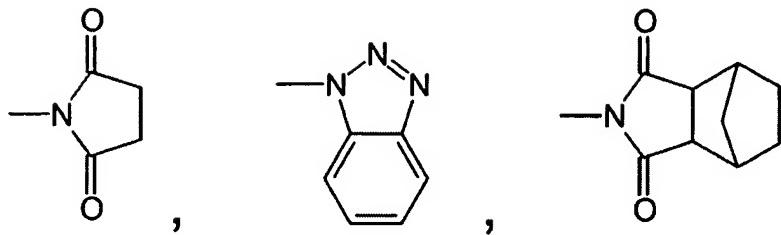
wherein M represents a transition metal; L<sub>1</sub> represents a ligand having a substituent: -R<sub>2</sub>-CO-OR<sub>1</sub>, where R<sub>2</sub> represents a phenylene group, R<sub>1</sub> represents H or an active ester-forming group; L<sub>2</sub> represents a ligand; m is a number of L<sub>2</sub>, indicating 0, 1, 2, 3, 4 or 5.

17. (Canceled).

18. (Currently Amended) The metal complex method for determining amino acid sequence of protein or peptide according to claim 17\_16, which wherein the metal complex is represented by the following general formula (II):



wherein M represents a transition metal; and R<sub>1</sub> represents H or an active ester-forming group represented by any of the following formula:



19. (Cancelled).

20. (Cancelled).

21. (Currently Amended) A method for determining amino acid sequence of protein or peptide, which comprises

reacting a metal complex which comprises a functional group which has a property of forming a covalent bond with an amino group of an N-terminal amino acid residue of protein or peptide or with a carboxyl group of a C-terminal amino acid residue of protein or peptide, with a protein or peptide (A) of which the amino acid sequence is to be determined, to form a derivative (B) of said metal complex where the covalent bond of the functional group of the metal complex with the amino group of the N-terminal amino acid residue of the protein or peptide (A) or with the carboxyl group of the C-terminal amino acid residue of protein or peptide (A) is formed, and

analyzing the derivative (B) of said metal complex through mass spectrometry to obtain mass spectrometry data of the derivative (B), and

determining the amino acid sequence of said protein or peptide from the mass spectrometry data,

wherein the derivative (B) comprises said metal complex covalently bonded via ~~a~~ the functional group on said metal complex to either the amino group of the N-terminal amino acid residue or the carboxyl group of the C-terminal amino acid residue of said protein or peptide (A).

22. (Cancelled).

23. (Canceled).

24. (Currently Amended) A method for determining amino acid sequence of protein or peptide, which comprises

reacting ~~the a metal complex according to claim 19~~ with a protein or peptide (A) of which the amino acid sequence is to be determined, to form a derivative (B) of said metal complex, ~~where the covalent bond of the functional group of the metal complex with the amino group of the N-terminal amino acid residue of the protein or peptide (A) or with the carboxyl group of the C-terminal amino acid residue of protein or peptide is formed, and~~

analyzing the derivative (B) through mass spectrometry to obtain mass spectrometry data of the derivative (B), and

determining the amino acid sequence of said protein or peptide from the mass spectrometry data,

wherein said metal complex comprises a functional group which has a property of forming a covalent bond with a carboxyl group of a C-terminal amino acid residue of protein or peptide,

wherein the derivative (B) comprises said metal complex covalently bonded via ~~a~~ the functional group on said metal complex to either the amino group of the N-terminal amino acid residue or the carboxyl group of the C-terminal amino acid residue of said protein or peptide (A),

wherein the covalent bond to be formed between the carboxyl group of the C-terminal amino acid residue of protein or peptide and the functional group is not cleaved in a stage of ionization in mass spectrometry,

wherein the metal complex is represented by the following formula (III):



wherein M represents a transition metal; L<sub>3</sub> represents a ligand having a substituent: -R<sub>2</sub>-NH<sub>2</sub> or -R<sub>2</sub>-NHNH<sub>2</sub>, where R<sub>2</sub> represents a phenylene group; L<sub>2</sub> represents a ligand; m is a number of L<sub>2</sub>, indicating 0, 1, 2, 3, 4 or 5.